



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Luo, Yuling
Xiomei, Xu
- (ii) TITLE OF INVENTION: Semaphorin K1
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 - (B) STREET: 75 DENISE DRIVE
 - (C) CITY: HILLSBOROUGH
 - (D) STATE: CALIFORNIA
 - (E) COUNTRY: USA
 - (F) ZIP: 94010
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/041,236
 - (B) FILING DATE: March 11, 1998
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: OSMAN, RICHARD A
 - (B) REGISTRATION NUMBER: 36,627
 - (C) REFERENCE/DOCKET NUMBER: EXEL98-001
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (650) 343-4341
 - (B) TELEFAX: (650) 343-4342

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2498 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..1902
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
- | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| CTG | CTG | CTG | CTG | CTC | TGG | GCG | GCC | GCC | GCC | TCC | GCC | CAG | GGC | CAC | CTA | 48 |
| Leu | Leu | Leu | Leu | Leu | Trp | Ala | Ala | Ala | Ala | Ser | Ala | Gln | Gly | His | Leu | |
| 1 | | | | 5 | | | | | | 10 | | | | | 15 | |
| AGG | AGC | GGA | CCC | CGC | ATC | TTC | GCC | GTC | TGG | AAA | GGC | CAT | GTA | GGG | CAG | 96 |
| Arg | Ser | Gly | Pro | Arg | Ile | Phe | Ala | Val | Trp | Lys | Gly | His | Val | Gly | Gln | |
| | | | 20 | | | | | | 25 | | | | | 30 | | |
| GAC | CGG | GTG | GAC | TTT | GGC | CAG | ACT | GAG | CCG | CAC | ACG | GTG | CTT | TTC | CAC | 144 |
| Asp | Arg | Val | Asp | Phe | Gly | Gln | Thr | Glu | Pro | His | Thr | Val | Leu | Phe | His | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| GAG | CCA | GGC | AGC | TCC | TCT | GTG | TGG | GTG | GGA | GGA | CGT | GGC | AAG | GTC | TAC | 192 |
| Glu | Pro | Gly | Ser | Ser | Ser | Val | Trp | Val | Gly | Gly | Arg | Gly | Lys | Val | Tyr | |
| | | 50 | | | | | 55 | | | | 60 | | | | | |
| CTC | TTT | GAC | TTC | CCC | GAG | GGC | AAG | AAC | GCA | TCT | GTG | CGC | ACG | GTG | AAT | 240 |
| Leu | Phe | Asp | Phe | Pro | Glu | Gly | Lys | Asn | Ala | Ser | Val | Arg | Thr | Val | Asn | |
| | | 65 | | | | 70 | | | | 75 | | | | | 80 | |
| ATC | GGC | TCC | ACA | AAG | GGG | TCC | TGT | CTG | GAT | AAG | CGG | GAC | TGC | GAG | AAC | 288 |
| Ile | Gly | Ser | Thr | Lys | Gly | Ser | Cys | Leu | Asp | Lys | Arg | Asp | Cys | Glu | Asn | |
| | | | 85 | | | | 90 | | | | | | 95 | | | |
| TAC | ATC | ACT | CTC | CTG | GAG | AGG | CGG | AGT | GAG | GGG | CTG | CTG | GCC | TGT | GGC | 336 |
| Tyr | Ile | Thr | Leu | Leu | Glu | Arg | Arg | Ser | Glu | Gly | Leu | Leu | Ala | Cys | Gly | |
| | | | 100 | | | | 105 | | | | | | 110 | | | |
| ACC | AAC | GCC | CGG | CAC | CCC | AGC | TGC | TGG | AAC | CTG | GTG | AAT | GGC | ACT | GTG | 384 |
| Thr | Asn | Ala | Arg | His | Pro | Ser | Cys | Trp | Asn | Leu | Val | Asn | Gly | Thr | Val | |

GTG	CCA	CTT	GGC	GAG	ATG	AGA	GGC	TAC	GCC	CCC	TTC	AGC	CCG	GAC	GAG	432
Val	Pro	Leu	Gly	Glu	Met	Arg	Gly	Tyr	Ala	Pro	Phe	Ser	Pro	Asp	Glu	
130						135					140					
AAC	TCC	CTG	GTT	CTG	TTT	GAA	GGG	GAC	GAG	GTG	TAT	TCC	ACC	ATC	CGG	480
Asn	Ser	Leu	Val	Leu	Phe	Glu	Gly	Asp	Glu	Val	Tyr	Ser	Thr	Ile	Arg	
145					150					155					160	
AAG	CAG	GAA	TAC	AAT	GGG	AAG	ATC	CCT	CGG	TTC	CGC	CGC	ATC	CGG	GGC	528
Lys	Gln	Glu	Tyr	Asn	Gly	Lys	Ile	Pro	Arg	Phe	Arg	Arg	Ile	Arg	Gly	
				165				170						175		
GAG	AGT	GAG	CTG	TAC	ACC	AGT	GAT	ACT	GTC	ATG	CAG	AAC	CCA	CAG	TTC	576
Glu	Ser	Glu	Leu	Tyr	Thr	Ser	Asp	Thr	Val	Met	Gln	Asn	Pro	Gln	Phe	
			180					185					190			
ATC	AAA	GCC	ACC	ATC	GTG	CAC	CAA	GAC	CAG	GCT	TAC	GAT	GAC	AAG	ATC	624
Ile	Lys	Ala	Thr	Ile	Val	His	Gln	Asp	Gln	Ala	Tyr	Asp	Asp	Lys	Ile	
	195					200					205					
TAC	TAC	TTC	TTC	CGA	GAG	GAC	AAT	CCT	GAC	AAG	AAT	CCT	GAG	GCT	CCT	672
Tyr	Tyr	Phe	Phe	Arg	Glu	Asp	Asn	Pro	Asp	Lys	Asn	Pro	Glu	Ala	Pro	
	210				215						220					
CTC	AAT	GTG	TCC	CGT	GTG	GCC	CAG	TTG	TGC	AGG	GGG	GAC	CAG	GGT	GGG	720
Leu	Asn	Val	Ser	Arg	Val	Ala	Gln	Leu	Cys	Arg	Gly	Asp	Gln	Gly	Gly	
225				230				235						240		
GAA	AGT	TCA	CTG	TCA	GTC	TCC	AAG	TGG	AAC	ACT	TTT	CTG	AAA	GCC	ATG	768
Glu	Ser	Ser	Leu	Ser	Val	Ser	Lys	Trp	Asn	Thr	Phe	Leu	Lys	Ala	Met	
			245					250					255			
CTG	GTA	TGC	AGT	GAT	GCT	GCC	ACC	AAC	AAG	AAC	TTC	AAC	AGG	CTG	CAA	816
Leu	Val	Cys	Ser	Asp	Ala	Ala	Thr	Asn	Lys	Asn	Phe	Asn	Arg	Leu	Gln	
			260			265					270					
GAC	GTC	TTC	CTG	CTC	CCT	GAC	CCC	AGC	GGC	CAG	TGG	AGG	GAC	ACC	AGG	864
Asp	Val	Phe	Leu	Leu	Pro	Asp	Pro	Ser	Gly	Gln	Trp	Arg	Asp	Thr	Arg	
	275				280						285					
GTC	TAT	GGT	GTT	TTC	TCC	AAC	CCC	TGG	AAC	TAC	TCA	GCC	GTC	TGT	GTG	912
Val	Tyr	Gly	Val	Phe	Ser	Asn	Pro	Trp	Asn	Tyr	Ser	Ala	Val	Cys	Val	
	290			295				300								
TAT	TCC	CTC	GGT	GAC	ATT	GAC	AAG	GTC	TTC	CGT	ACC	TCC	TCA	CTC	AAG	960
Tyr	Ser	Leu	Gly	Asp	Ile	Asp	Lys	Val	Phe	Arg	Thr	Ser	Ser	Leu	Lys	
305				310				315						320		
GGC	TAC	CAC	TCA	AGC	CTT	CCC	AAC	CCG	CGG	CCT	GGC	AAG	TGC	CTC	CCA	1008
Gly	Tyr	His	Ser	Ser	Leu	Pro	Asn	Pro	Arg	Pro	Gly	Lys	Cys	Leu	Pro	
			325					330					335			
GAC	CAG	CAG	CCG	ATA	CCC	ACA	GAG	ACC	TTC	CAG	GTG	GCT	GAC	CGT	CAC	1056
Asp	Gln	Gln	Pro	Ile	Pro	Thr	Glu	Thr	Phe	Gln	Val	Ala	Asp	Arg	His	
			340					345					350			
CCA	GAG	GTG	GCG	CAG	AGG	GTG	GAG	CCC	ATG	GGG	CCT	CTG	AAG	ACG	CCA	1104
Pro	Glu	Val	Ala	Gln	Arg	Val	Glu	Pro	Met	Gly	Pro	Leu	Lys	Thr	Pro	
	355					360					365					
TTG	TTC	CAC	TCT	AAA	TAC	CAC	TAC	CAG	AAA	GTG	GCC	GTC	CAC	CGC	ATG	1152
Leu	Phe	His	Ser	Lys	Tyr	His	Tyr	Gln	Lys	Val	Ala	Val	His	Arg	Met	
	370				375						380					
CAA	GCC	AGC	CAC	GGG	GAG	ACC	TTT	CAT	GTG	CTT	TAC	CTA	ACT	ACA	GAC	1200
Gln	Ala	Ser	His	Gly	Glu	Thr	Phe	His	Val	Leu	Tyr	Leu	Thr	Thr	Asp	
385				390				395						400		
AGG	GGC	ACT	ATC	CAC	AAG	GTG	GTG	GAA	CCG	GGG	GAG	CAG	GAG	CAC	AGC	1248
Arg	Gly	Thr	Ile	His	Lys	Val	Val	Glu	Pro	Gly	Glu	Gln	Glu	His	Ser	
			405					410					415			
TTC	GCC	TTC	AAC	ATC	ATG	GAG	ATC	CAG	CCC	TTC	CGC	CGC	GCG	GCT	GCC	1296
Phe	Ala	Phe	Asn	Ile	Met	Glu	Ile	Gln	Pro	Phe	Arg	Arg	Ala	Ala	Ala	
			420					425					430			
ATC	CAG	ACC	ATG	TCG	CTG	GAT	GCT	GAG	CGG	AGG	AAG	CTG	TAT	GTG	AGC	1344
Ile	Gln	Thr	Met	Ser	Leu	Asp	Ala	Glu	Arg	Arg	Lys	Leu	Tyr	Val	Ser	
		435				440						445				
TCC	CAG	TGG	GAG	GTG	AGC	CAG	GTG	CCC	CTG	GAC	CTG	TGT	GAG	GTC	TAT	1392
Ser	Gln	Trp	Glu	Val	Ser	Gln	Val	Pro	Leu	Asp	Leu	Cys	Glu	Val	Tyr	
	450					455					460					

GGC GGG GGC TGC CAC GGT TGC CTC ATG TCC CGA GAC CCC TAC TGC GGC	1440
Gly Gly Gly Cys His Gly Cys Leu Met Ser Arg Asp Pro Tyr Cys Gly	
465 470 475 480	
TGG GAC CAA GGC CGC TGC ATC TCC ATC TAC AGC TCC GAA CGG TCA GTG	1488
Trp Asp Gln Gly Arg Cys Ile Ser Ile Tyr Ser Ser Glu Arg Ser Val	
485 490 495	
CTG CAA TCC ATT AAT CCA GCC GAG CCA CAC AAG GAG TGT CCC AAC CCC	1536
Leu Gln Ser Ile Asn Pro Ala Glu Pro His Lys Glu Cys Pro Asn Pro	
500 505 510	
AAA CCA GAC AAG GCC CCA CTG CAG AAG GTT TCC CTG GCC CCA AAC TCT	1584
Lys Pro Asp Lys Ala Pro Leu Gln Lys Val Ser Leu Ala Pro Asn Ser	
515 520 525	
CGC TAC TAC CTG AGC TGC CCC ATG GAA TCC CGC CAC GCC ACC TAC TCA	1632
Arg Tyr Tyr Leu Ser Cys Pro Met Glu Ser Arg His Ala Thr Tyr Ser	
530 535 540	
TGG CGC CAC AAG GAG AAC GTG GAG CAG AGC TGC GAA CCT GGT CAC CAG	1680
Trp Arg His Lys Glu Asn Val Glu Gln Ser Cys Glu Pro Gly His Gln	
545 550 555 560	
AGC CCC AAC TGC ATC CTG TTC ATC GAG AAC CTC ACG GCG CAG CAG TAC	1728
Ser Pro Asn Cys Ile Leu Phe Ile Glu Asn Leu Thr Ala Gln Gln Tyr	
565 570 575	
GGC CAC TAC TTC TGC GAG GCC CAG GAG GGC TCC TAC TTC CGC GAG GCT	1776
Gly His Tyr Phe Cys Glu Ala Gln Glu Gly Ser Tyr Phe Arg Glu Ala	
580 585 590	
CAG CAC TGG CAG CTG CTG CCC GAG GAC GGC ATC ATG GCC GAG CAC CTG	1824
Gln His Trp Gln Leu Leu Pro Glu Asp Gly Ile Met Ala Glu His Leu	
595 600 605	
CTG GGT CAT GCC TGT GCC CTG GCC GCC TCC CTC TGG CTG GGG GTG CTG	1872
Leu Gly His Ala Cys Ala Leu Ala Ala Ser Leu Trp Leu Gly Val Leu	
610 615 620	
CCC ACA CTC ACT CTT GGC TTG CTG GTC CAC TAGGGCCTCC CGAGGCTGGG	1922
Pro Thr Leu Thr Leu Gly Leu Leu Val His	
625 630	
CATGCCTCAG GCTTCTGCAG CCCAGGGCAC TAAAACGTCT CACACTCAGA GCCGGCTGGC	1982
CCGGGAGCTC CTTGCCTGCC ATTTTTTCCA GGGGACAGAA TAACCCAGTG GAGGATGCCA	2042
GGCCTGGAGA CGTCCAGCCG CAGGCGGCTG CTGGGCCCCA GGATGGTGAG	2102
GGGCTGAGAA TGAGGGCACC GACTGTGAAG CTGGGGCATC GATGACCCAA GACTTTATTT	2162
TTTGGAAAAT ATTTTTTCAGA CTCCTCAAAC TTGACTAAAT GCAGCGATGC TCCCAGCCCA	2222
AGAGCCCATG GGTCGGGGAG TGGGTTTGGG TAGGAGAGCT GGGATTCCAT CTCGACCCTG	2282
GGGCTGAGGC CTGAGTCCTT TTGGATTCTT GGTACCCACA TTGCCTCCTT CCCCTCCTTT	2342
TTTCAGGGGT GGGTGGTTGG TGTTCTTGAA GACCCAGGGA TACCCTTTGT CCAGCCCTGT	2402
CCTTGGCAGC TCCCTTTTTG GTCCTGGGTC CCACAGGACA GCCGCCTTGC ATGTTTATTG	2462
AAGGATGTTT GCTTTCGGA CGGAAGGACG GAAAAA	2498

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 634 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Leu	Leu	Leu	Leu	Leu	Trp	Ala	Ala	Ala	Ala	Ser	Ala	Gln	Gly	His	Leu
1				5					10					15	
Arg	Ser	Gly	Pro	Arg	Ile	Phe	Ala	Val	Trp	Lys	Gly	His	Val	Gly	Gln
			20					25					30		
Asp	Arg	Val	Asp	Phe	Gly	Gln	Thr	Glu	Pro	His	Thr	Val	Leu	Phe	His
		35					40					45			
Glu	Pro	Gly	Ser	Ser	Ser	Val	Trp	Val	Gly	Gly	Arg	Gly	Lys	Val	Tyr
	50					55				60					
Leu	Phe	Asp	Phe	Pro	Glu	Gly	Lys	Asn	Ala	Ser	Val	Arg	Thr	Val	Asn
	65				70				75						80
Ile	Gly	Ser	Thr	Lys	Gly	Ser	Cys	Leu	Asp	Lys	Arg	Asp	Cys	Glu	Asn
			85					90						95	
Tyr	Ile	Thr	Leu	Leu	Glu	Arg	Arg	Ser	Glu	Gly	Leu	Leu	Ala	Cys	Gly

			100					105					110		
Thr	Asn	Ala	Arg	His	Pro	Ser	Cys	Trp	Asn	Leu	Val	Asn	Gly	Thr	Val
		115					120					125			
Val	Pro	Leu	Gly	Glu	Met	Arg	Gly	Tyr	Ala	Pro	Phe	Ser	Pro	Asp	Glu
	130					135					140				
Asn	Ser	Leu	Val	Leu	Phe	Glu	Gly	Asp	Glu	Val	Tyr	Ser	Thr	Ile	Arg
145					150					155					160
Lys	Gln	Glu	Tyr	Asn	Gly	Lys	Ile	Pro	Arg	Phe	Arg	Arg	Ile	Arg	Gly
				165					170					175	
Glu	Ser	Glu	Leu	Tyr	Thr	Ser	Asp	Thr	Val	Met	Gln	Asn	Pro	Gln	Phe
			180					185					190		
Ile	Lys	Ala	Thr	Ile	Val	His	Gln	Asp	Gln	Ala	Tyr	Asp	Asp	Lys	Ile
		195					200					205			
Tyr	Tyr	Phe	Phe	Arg	Glu	Asp	Asn	Pro	Asp	Lys	Asn	Pro	Glu	Ala	Pro
	210					215					220				
Leu	Asn	Val	Ser	Arg	Val	Ala	Gln	Leu	Cys	Arg	Gly	Asp	Gln	Gly	Gly
225					230					235					240
Glu	Ser	Ser	Leu	Ser	Val	Ser	Lys	Trp	Asn	Thr	Phe	Leu	Lys	Ala	Met
				245					250					255	
Leu	Val	Cys	Ser	Asp	Ala	Ala	Thr	Asn	Lys	Asn	Phe	Asn	Arg	Leu	Gln
			260					265					270		
Asp	Val	Phe	Leu	Leu	Pro	Asp	Pro	Ser	Gly	Gln	Trp	Arg	Asp	Thr	Arg
		275					280					285			
Val	Tyr	Gly	Val	Phe	Ser	Asn	Pro	Trp	Asn	Tyr	Ser	Ala	Val	Cys	Val
	290					295					300				
Tyr	Ser	Leu	Gly	Asp	Ile	Asp	Lys	Val	Phe	Arg	Thr	Ser	Ser	Leu	Lys
305					310					315					320
Gly	Tyr	His	Ser	Ser	Leu	Pro	Asn	Pro	Arg	Pro	Gly	Lys	Cys	Leu	Pro
				325					330					335	
Asp	Gln	Gln	Pro	Ile	Pro	Thr	Glu	Thr	Phe	Gln	Val	Ala	Asp	Arg	His
			340					345					350		
Pro	Glu	Val	Ala	Gln	Arg	Val	Glu	Pro	Met	Gly	Pro	Leu	Lys	Thr	Pro
		355					360					365			
Leu	Phe	His	Ser	Lys	Tyr	His	Tyr	Gln	Lys	Val	Ala	Val	His	Arg	Met
	370					375					380				
Gln	Ala	Ser	His	Gly	Glu	Thr	Phe	His	Val	Leu	Tyr	Leu	Thr	Thr	Asp
385					390					395					400
Arg	Gly	Thr	Ile	His	Lys	Val	Val	Glu	Pro	Gly	Glu	Gln	Glu	His	Ser
				405					410					415	
Phe	Ala	Phe	Asn	Ile	Met	Glu	Ile	Gln	Pro	Phe	Arg	Arg	Ala	Ala	Ala
			420					425					430		
Ile	Gln	Thr	Met	Ser	Leu	Asp	Ala	Glu	Arg	Arg	Lys	Leu	Tyr	Val	Ser
		435					440					445			
Ser	Gln	Trp	Glu	Val	Ser	Gln	Val	Pro	Leu	Asp	Leu	Cys	Glu	Val	Tyr
	450														

610
Pro Thr Leu Thr Leu Gly Leu Leu Val His
625 630

620

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1818 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1818

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG GGC ACT TTG TGT GTT AGT ATT AGA TTA CTG ATG ATT TTA TCA GCC	48
Met Gly Thr Leu Cys Val Ser Ile Arg Leu Leu Met Ile Leu Ser Ala	
635 640 645 650	
ATC ACA GCT GCT AAA TCT CGG TTT ATA GAT AAG CCA AGG CTG ATT GTT	96
Ile Thr Ala Ala Lys Ser Arg Phe Ile Asp Lys Pro Arg Leu Ile Val	
655 660 665	
AAC CTA ACT GAT GGG TTT GGA CAG CAC CGG TTT TTT GGA CCC CAG GAA	144
Asn Leu Thr Asp Gly Phe Gly Gln His Arg Phe Phe Gly Pro Gln Glu	
670 675 680	
CCA CAC ACT GTG CTT TTT CAC AGC CTC AAC TCT TCA GAC GTA TAT GTG	192
Pro His Thr Val Leu Phe His Ser Leu Asn Ser Ser Asp Val Tyr Val	
685 690 695	
GGA GGT AAT AAT ACC ATC TAT TTG TTT GAT TTT GCT CAC AGC TCC AAC	240
Gly Gly Asn Asn Thr Ile Tyr Leu Phe Asp Phe Ala His Ser Ser Asn	
700 705 710	
GCA TCC ACA GCT TTG ATA AAC ATA ACT AGC ACA CAT AAT ACC CAC CGG	288
Ala Ser Thr Ala Leu Ile Asn Ile Thr Ser Thr His Asn Thr His Arg	
715 720 725 730	
TTA TCT AGT ACC TGC GAA AAC TTT ATA ACT CTG CTT CAT AAC CAG ACA	336
Leu Ser Ser Thr Cys Glu Asn Phe Ile Thr Leu Leu His Asn Gln Thr	
735 740 745	
GAT GGG CTG CTA GCT TGT GGT ACT AAC TCA CAG AAA CCC AGC TGC TGG	384
Asp Gly Leu Leu Ala Cys Gly Thr Asn Ser Gln Lys Pro Ser Cys Trp	
750 755 760	
CTG ATA AAC AAC CTA ACA ACT CAA TTT TTG GGG CCA AAA CTA GGC TTA	432
Leu Ile Asn Asn Leu Thr Thr Gln Phe Leu Gly Pro Lys Leu Gly Leu	
765 770 775	
GCC CCC TTC TCA CCA TCA TCT GGC AAT CTG GTG CTG TTT GAC CAG AAT	480
Ala Pro Phe Ser Pro Ser Ser Gly Asn Leu Val Leu Phe Asp Gln Asn	
780 785 790	
GAC ACC TAT TCC ACC ATT AAC CTC TAC AAG AGC CTC AGT GGC TCT CAC	528
Asp Thr Tyr Ser Thr Ile Asn Leu Tyr Lys Ser Leu Ser Gly Ser His	
795 800 805 810	
AAG TTT AGG AGG ATC GCT GGC CAA GTA GAA CTA TAC ACG AGT GAC ACC	576
Lys Phe Arg Arg Ile Ala Gly Gln Val Glu Leu Tyr Thr Ser Asp Thr	
815 820 825	
GCC ATG CAC CGG CCA CAG TTT GTC CAG GCA ACA GCT GTG CAT AAA AAT	624
Ala Met His Arg Pro Gln Phe Val Gln Ala Thr Ala Val His Lys Asn	
830 835 840	
GAA TCT TAT GAT GAT AAA ATC TAC TTT TTC TTT CAA GAA AAC AGC CAC	672
Glu Ser Tyr Asp Asp Lys Ile Tyr Phe Phe Phe Gln Glu Asn Ser His	
845 850 855	
AGT GAC TTC AAA CAG TTT CCA CAT ACT GTA CCT AGA GTG GGG CAG GTG	720
Ser Asp Phe Lys Gln Phe Pro His Thr Val Pro Arg Val Gly Gln Val	
860 865 870	
TGC TCT AGT GAT CAA GGT GGG GAG AGC TCC CTG TCT GTC TAC AAG TGG	768
Cys Ser Ser Asp Gln Gly Gly Glu Ser Ser Leu Ser Val Tyr Lys Trp	
875 880 885 890	
ACC ACC TTT TTA AAA GCC AGA CTG GCG TGT GTA GAC TAT GAT ACT GGA	816

Thr	Thr	Phe	Leu	Lys	Ala	Arg	Leu	Ala	Cys	Val	Asp	Tyr	Asp	Thr	Gly	
			895						900					905		
AGA	ATC	TAC	AAT	GAG	CTA	CAA	GAT	ATT	TTC	ATC	TGG	CAA	GCC	CCA	GAG	864
Arg	Ile	Tyr	Asn	Glu	Leu	Gln	Asp	Ile	Phe	Ile	Trp	Gln	Ala	Pro	Glu	
			910						915				920			
AAC	AGC	TGG	GAA	GAG	ACT	CTC	ATC	TAT	GGA	CTT	TTT	TTG	AGC	CCG	TGG	912
Asn	Ser	Trp	Glu	Glu	Thr	Leu	Ile	Tyr	Gly	Leu	Phe	Leu	Ser	Pro	Trp	
		925					930					935				
AAC	TTT	TCT	GCG	GTC	TGT	GTG	TTT	ACT	GTA	AAG	GAC	ATT	GAC	CAT	GTG	960
Asn	Phe	Ser	Ala	Val	Cys	Val	Phe	Thr	Val	Lys	Asp	Ile	Asp	His	Val	
	940					945					950					
TTT	AAG	ACA	TCC	AAG	TTA	AAA	AAT	TAT	CAT	CAT	AAA	CTC	CCC	ACA	CCT	1008
Phe	Lys	Thr	Ser	Lys	Leu	Lys	Asn	Tyr	His	His	Lys	Leu	Pro	Thr	Pro	
955					960					965					970	
AGA	CCA	GGG	CAA	TGC	ATG	AAG	AAC	CAT	CAG	CAT	GTT	CCC	ACA	GAA	ACC	1056
Arg	Pro	Gly	Gln	Cys	Met	Lys	Asn	His	Gln	His	Val	Pro	Thr	Glu	Thr	
			975						980					985		
TTT	CAG	GTT	GCT	GAC	AGA	TAT	CCA	GAA	GTT	GCA	GAT	CCT	GTA	TAT	CAG	1104
Phe	Gln	Val	Ala	Asp	Arg	Tyr	Pro	Glu	Val	Ala	Asp	Pro	Val	Tyr	Gln	
		990					995					1000				
AAG	AAC	AAT	GCC	ATG	TTT	CCA	ATA	ATT	CAG	TCA	AAA	TAT	ATC	TAC	ACC	1152
Lys	Asn	Asn	Ala	Met	Phe	Pro	Ile	Ile	Gln	Ser	Lys	Tyr	Ile	Tyr	Thr	
	1005					1010					1015					
AAA	CTA	CTT	GTT	TAT	AGG	GTA	GAG	TAT	GGA	GGT	GTT	TTT	TGG	GCA	ACT	1200
Lys	Leu	Leu	Val	Tyr	Arg	Val	Glu	Tyr	Gly	Gly	Val	Phe	Trp	Ala	Thr	
	1020					1025				1030						
ATT	TTT	TAC	CTC	ACT	ACC	ATC	AAA	GGG	ACT	ATT	CAT	ATA	TAT	GTG	AGG	1248
Ile	Phe	Tyr	Leu	Thr	Thr	Ile	Lys	Gly	Thr	Ile	His	Ile	Tyr	Val	Arg	
1035					1040				1045					1050		
TAT	GAA	GAT	TCC	AAC	TCT	ACA	ACA	GCT	CTC	AAC	ATT	TTA	GAG	ATA	AAT	1296
Tyr	Glu	Asp	Ser	Asn	Ser	Thr	Thr	Ala	Leu	Asn	Ile	Leu	Glu	Ile	Asn	
			1055					1060				1065				
CCC	TTT	CAG	AAG	CCA	GCC	CCC	ATA	CAG	AAT	ATT	CTT	TTA	GAT	AAT	ACA	1344
Pro	Phe	Gln	Lys	Pro	Ala	Pro	Ile	Gln	Asn	Ile	Leu	Leu	Asp	Asn	Thr	
		1070					1075				1080					
AAT	CTA	AAG	CTT	TAT	GTA	AAT	TCA	GAG	TGG	GAG	GTG	AGT	GAG	GTG	CCA	1392
Asn	Leu	Lys	Leu	Tyr	Val	Asn	Ser	Glu	Trp	Glu	Val	Ser	Glu	Val	Pro	
	1085					1090					1095					
TTA	GAC	CTA	TGT	TCA	GTG	TAT	GGG	AAT	GAT	TGT	TTC	AGC	TGT	TTT	ATG	1440
Leu	Asp	Leu	Cys	Ser	Val	Tyr	Gly	Asn	Asp	Cys	Phe	Ser	Cys	Phe	Met	
	1100				1105					1110						
TCA	AGG	GAT	CCC	CTG	TGC	ACA	TGG	TAT	AAC	AAC	ACC	TGT	TCC	TTT	AAA	1488
Ser	Arg	Asp	Pro	Leu	Cys	Thr	Trp	Tyr	Asn	Asn	Thr	Cys	Ser	Phe	Lys	
1115				1120					1125					1130		
CAG	AGA	GTA	TCT	GTT	GAA	ACC	GGT	GGT	CCA	GCT	AAC	CGC	ACC	CTT	TCA	1536
Gln	Arg	Val	Ser	Val	Glu	Thr	Gly	Gly	Pro	Ala	Asn	Arg	Thr	Leu	Ser	
			1135				1140					1145				
GAA	ATG	TGT	GGT	GAC	CAC	TAT	GCT	CCA	ACT	GTG	GTT	AAG	CAT	CAA	GTT	1584
Glu	Met	Cys	Gly	Asp	His	Tyr	Ala	Pro	Thr	Val	Val	Lys	His	Gln	Val	
		1150					1155					1160				
TCT	ATA	CCT	CTA	TTA	TCT	AAT	TCT	TAT	TTG	TCC	TGC	CCA	GCA	GTC	TCA	1632
Ser	Ile	Pro	Leu	Leu	Ser	Asn	Ser	Tyr	Leu	Ser	Cys	Pro	Ala	Val	Ser	
	1165					1170					1175					
AAC	CAC	GCT	GAC	TAC	TTT	TGG	ACT	AAA	GAT	GGT	TTC	ACA	GAA	AAA	AGA	1680
Asn	His	Ala	Asp	Tyr	Phe	Trp	Thr	Lys	Asp	Gly	Phe	Thr	Glu	Lys	Arg	
	1180				1185					1190						
TGC	CAT	GTC	AAA	ACA	CAC	AAA	AAT	GAC	TGC	ATC	TTG	CTT	ATA	GCT	AAC	1728
Cys	His	Val	Lys	Thr	His	Lys	Asn	Asp	Cys	Ile	Leu	Leu	Ile	Ala	Asn	
1195				1200					1205					1210		
AGC	ACG	ACA	GCC	ACT	AAT	GGA	ACC	CAC	GTG	TGC	AAC	ATG	AAA	GAA	GAT	1776
Ser	Thr	Thr	Ala	Thr	Asn	Gly	Thr	His	Val	Cys	Asn	Met	Lys	Glu	Asp	
			1215					1220				1225				
TCG	GTG	ACA	GTG	AAA	CTG	TTA	GAG	GTG	AAT	GTG	ACA	CTG	ATG			1818
Ser	Val	Thr	Val	Lys	Leu	Leu	Glu	Val	Asn	Val	Thr	Leu	Met			

1230

1235

1240

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 606 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Gly	Thr	Leu	Cys	Val	Ser	Ile	Arg	Leu	Leu	Met	Ile	Leu	Ser	Ala
1				5					10					15	
Ile	Thr	Ala	Ala	Lys	Ser	Arg	Phe	Ile	Asp	Lys	Pro	Arg	Leu	Ile	Val
		20						25					30		
Asn	Leu	Thr	Asp	Gly	Phe	Gly	Gln	His	Arg	Phe	Phe	Gly	Pro	Gln	Glu
		35					40					45			
Pro	His	Thr	Val	Leu	Phe	His	Ser	Leu	Asn	Ser	Ser	Asp	Val	Tyr	Val
	50					55					60				
Gly	Gly	Asn	Asn	Thr	Ile	Tyr	Leu	Phe	Asp	Phe	Ala	His	Ser	Ser	Asn
65					70					75					80
Ala	Ser	Thr	Ala	Leu	Ile	Asn	Ile	Thr	Ser	Thr	His	Asn	Thr	His	Arg
			85					90					95		
Leu	Ser	Ser	Thr	Cys	Glu	Asn	Phe	Ile	Thr	Leu	Leu	His	Asn	Gln	Thr
			100					105					110		
Asp	Gly	Leu	Leu	Ala	Cys	Gly	Thr	Asn	Ser	Gln	Lys	Pro	Ser	Cys	Trp
		115					120					125			
Leu	Ile	Asn	Asn	Leu	Thr	Thr	Gln	Phe	Leu	Gly	Pro	Lys	Leu	Gly	Leu
	130						135				140				
Ala	Pro	Phe	Ser	Pro	Ser	Ser	Gly	Asn	Leu	Val	Leu	Phe	Asp	Gln	Asn
145					150					155					160
Asp	Thr	Tyr	Ser	Thr	Ile	Asn	Leu	Tyr	Lys	Ser	Leu	Ser	Gly	Ser	His
			165					170					175		
Lys	Phe	Arg	Arg	Ile	Ala	Gly	Gln	Val	Glu	Leu	Tyr	Thr	Ser	Asp	Thr
		180					185						190		
Ala	Met	His	Arg	Pro	Gln	Phe	Val	Gln	Ala	Thr	Ala	Val	His	Lys	Asn
	195						200					205			
Glu	Ser	Tyr	Asp	Asp	Lys	Ile	Tyr	Phe	Phe	Phe	Gln	Glu	Asn	Ser	His
	210					215					220				
Ser	Asp	Phe	Lys	Gln	Phe	Pro	His	Thr	Val	Pro	Arg	Val	Gly	Gln	Val
225					230					235					240
Cys	Ser	Ser	Asp	Gln	Gly	Gly	Glu	Ser	Ser	Leu	Ser	Val	Tyr	Lys	Trp
			245						250				255		
Thr	Thr	Phe	Leu	Lys	Ala	Arg	Leu	Ala	Cys	Val	Asp	Tyr	Asp	Thr	Gly
		260					265						270		
Arg	Ile	Tyr	Asn	Glu	Leu	Gln	Asp	Ile	Phe	Ile	Trp	Gln	Ala	Pro	Glu
	275						280					285			
Asn	Ser	Trp	Glu	Glu	Thr	Leu	Ile	Tyr	Gly	Leu	Phe	Leu	Ser	Pro	Trp
	290					295					300				
Asn	Phe	Ser	Ala	Val	Cys	Val	Phe	Thr	Val	Lys	Asp	Ile	Asp	His	Val
305					310					315					320
Phe	Lys	Thr	Ser	Lys	Leu	Lys	Asn	Tyr	His	His	Lys	Leu	Pro	Thr	Pro
			325						330				335		
Arg	Pro	Gly	Gln	Cys	Met	Lys	Asn	His	Gln	His	Val	Pro	Thr	Glu	Thr
		340						345					350		
Phe	Gln	Val	Ala	Asp	Arg	Tyr	Pro	Glu	Val	Ala	Asp	Pro	Val	Tyr	Gln
	355						360				365				
Lys	Asn	Asn	Ala	Met	Phe	Pro	Ile	Ile	Gln	Ser	Lys	Tyr	Ile	Tyr	Thr
	370					375					380				
Lys	Leu	Leu	Val	Tyr	Arg	Val	Glu	Tyr	Gly	Gly	Val	Phe	Trp	Ala	Thr
385					390					395					400
Ile	Phe	Tyr	Leu	Thr	Ile	Lys	Gly	Thr	Ile	His	Ile	Tyr	Val	Arg	
			405					410					415		
Tyr	Glu	Asp	Ser	Asn	Ser	Thr	Thr	Ala	Leu	Asn	Ile	Leu	Glu	Ile	Asn
		420						425					430		
Pro	Phe	Gln	Lys	Pro	Ala	Pro	Ile	Gln	Asn	Ile	Leu	Leu	Asp	Asn	Thr

435					440					445					
Asn	Leu	Lys	Leu	Tyr	Val	Asn	Ser	Glu	Trp	Glu	Val	Ser	Glu	Val	Pro
450						455						460			
Leu	Asp	Leu	Cys	Ser	Val	Tyr	Gly	Asn	Asp	Cys	Phe	Ser	Cys	Phe	Met
465						470						475			480
Ser	Arg	Asp	Pro	Leu	Cys	Thr	Trp	Tyr	Asn	Asn	Thr	Cys	Ser	Phe	Lys
				485					490					495	
Gln	Arg	Val	Ser	Val	Glu	Thr	Gly	Gly	Pro	Ala	Asn	Arg	Thr	Leu	Ser
			500					505						510	
Glu	Met	Cys	Gly	Asp	His	Tyr	Ala	Pro	Thr	Val	Val	Lys	His	Gln	Val
		515					520					525			
Ser	Ile	Pro	Leu	Leu	Ser	Asn	Ser	Tyr	Leu	Ser	Cys	Pro	Ala	Val	Ser
	530					535					540				
Asn	His	Ala	Asp	Tyr	Phe	Trp	Thr	Lys	Asp	Gly	Phe	Thr	Glu	Lys	Arg
545					550					555					560
Cys	His	Val	Lys	Thr	His	Lys	Asn	Asp	Cys	Ile	Leu	Leu	Ile	Ala	Asn
				565					570					575	
Ser	Thr	Thr	Ala	Thr	Asn	Gly	Thr	His	Val	Cys	Asn	Met	Lys	Glu	Asp
			580					585					590		
Ser	Val	Thr	Val	Lys	Leu	Leu	Glu	Val	Asn	Val	Thr	Leu	Met		
		595					600					605			